GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 31, 2003, 13:09:31 ; Search time 83 Seconds
(without alignments)
1005.906 Million cell updates/sec

Title: US-10-082-894-2
Perfect score: 2786
Sequence: 1 MDKYQNVQQKVCLVVIDGWG.....LMGLPVPPEMDGVPLLEQRG 526

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1141.5	41.0	510	23	ABB48814	Listeria monocytog
2	996	35.8	491	19	AAW98438	H. pylori GHPO 476
3	992	35.6	505	22	AAG82563	S. epidermidis ope
4	992	35.6	517	23	ABP40599	Staphylococcus epi
5	736.5	26.4	557	18	AAW28504	Mugwort grass poll
6	729	26.2	560	21	AAG38644	Arabidopsis thalia
7	706	25.3	557	21	AAG26479	Arabidopsis thalia
8	703	25.2	560	18	AAW28505	Mugwort grass poll
9	696	25.0	556	18	AAW28502	Timothy grass poll
10	694	24.9	555	18	AAW28503	Timothy grass poll
11	687	24.7	575	21	AAG30862	Arabidopsis thalia
12	686	24.6	530	18	AAW28501	Birch pollen co-fa
13	657	23.6	511	21	AAG38645	Arabidopsis thalia
14	647	23.2	510	21	AAG26480	Arabidopsis thalia
15	628	22.5	528	21	AAG30863	Arabidopsis thalia
16	612	22.0	482	21	AAG38646	Arabidopsis thalia
17	605	21.7	481	21	AAG26481	Arabidopsis thalia
18	586	21.0	499	21	AAG30864	Arabidopsis thalia
19	568.5	20.4	425	22	ABG21560	Novel human diagno
20	466	16.7	424	21	AAG27964	Arabidopsis thalia
21	425.5	15.3	353	21	AAG27965	Arabidopsis thalia
22	419.5	15.1	349	21	AAG27966	Arabidopsis thalia
23	333	12.0	161	19	AAW82632	Ehrlichia sp. HGE-
24	333	12.0	161	21	AAY78558	Ehrlichia antigen
25	333	12.0	161	23	ABG93405	Ehrlichia antigen
26	333	12.0	161	23	AAU73202	Human granulocytic
27	221	7.9	150	21	AAG32720	Zea mays protein f
28	214	7.7	136	21	AAG44003	Zea mays protein f
29	195	7.0	84	23	ABU50962	Helicobacter pylor
30	179	6.4	128	21	AAG19053	Zea mays protein f
31	179	6.4	166	21	AAG19052	Zea mays protein f
32	164	5.9	98	21	AAG12425	Zea mays protein f
33	160.5	5.8	74	23	ABP02681	Human ORFX protein
34	159.5	5.7	61	23	ABP33773	Human ORF2746 prot
35	156	5.6	102	21	AAG32721	Zea mays protein f
36	154	5.5	107	21	AAG12364	Zea mays protein f
37	149	5.3	91	21	AAG44004	Zea mays protein f
38	147.5	5.3	102	18	AAW28210	Amino acid sequenc
39	121	4.3	413	22	AAB96790	Putative P. abyssi
40	114	4.1	83	21	AAG19054	Zea mays protein f
41	110	3.9	431	22	AAE01521	Human gene 5 encod
42	110	3.9	709	22	AAE00435	C. elegans sulfata
43	110	3.9	880	22	ABB58897	Drosophila melanog
44	110	3.9	896	22	AAM24250	Human EST encoded
45	110	3.9	1089	21	AAY99369	Human PRO1249 (UNQ

ALIGNMENTS

RESULT 1
ABB48814
ID ABB48814 standard; Protein; 510 AA.
XX
AC ABB48814;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1518.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;

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PI   Rose M,  Voss H;
XX
DR   WPI; 2002-010914/01.
XX
PT   Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT   and prevention of Listeria and related bacterial infections, and
PT   related polypeptides  -
XX
PS   Claim 6; SEQ ID No 1519; 192pp; French.
XX
CC   The present invention relates to the genome sequence of Listeria
CC   monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC   it are useful for selecting probes and primers for detecting genes in L.
CC   monocytogenes and related organisms, and for studying genetic
CC   polymorphisms and other genomes. The present sequence is a protein
CC   encoded by the genome sequence of the present invention. Proteins
CC   expressed from the genome sequence are useful for raising specific
CC   antibodies, identification of L. monocytogenes and related organisms, and
CC   for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC   B12. The genome sequence and proteins encoded by it are also useful for
CC   selecting compounds that regulate gene expression and cell replication
CC   and modulate L. monocytogenes-related diseases. In addition, the genome
CC   sequence and proteins encoded by it are useful in pharmaceutical and
CC   vaccines compositions for the treatment or prevention of infections by L.
CC   monocytogenes and related organisms.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   510 AA;
```

Query Match 41.0%; Score 1141.5; DB 23; Length 510;
Best Local Similarity 44.0%; Pred. No. 3.6e-105;
Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7;

```
Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSGNWQ-----KLEAHGLHVGLPEGLMGN 65
Db          6 VAIIILDGFGKRAETVGNAVAQANKPNFDRY----WADFPHGELKAAGLDVGLPEGQMGN 61

Qy         66 SEVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGG 125
Db         62 SEVGHTNIGAGRIVYQSLTRIDKAIEEGEFQENKALNNAFTHTKENNSDLHLFGLLSDGG 121

Qy        126 VHSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKYGELAT 185
Db        122 VHSHINHLVALLETAKDKGVKNVYIHAFLDGRDVAPQSSLEYLETLQKAISDLNYGAIAT 181

Qy        186 ITGRYYAMDRDKRWERIKMAYEAIVGGIGQKATVDKAVDVVRERYAQSETDEFLKPIVFS 245
Db        182 VSGRFYAMDRDKRWERVEKAYKAIVSAEGEK--FEDPIELVKASYANDKNDEFVVPAIIT 239

Qy        246 DDGR----VKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYNK 301
Db        240 KDGKPVATVKDNDAVIFFNFRPDRAIQLSNAFTDKEWDHFDRGADHPKNIKFVTMTLYNP 299

Qy        302 EFPFPSLFPPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQDEERCMV 361
Db        300 SIDAEVAFEPIEMKNVIGEVLSNEGLSQLRIAETEKYPHVTFFMNGGRNEEFPGENRILI 359

Qy        362 PSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQ 421
Db        360 NSPK-VETYDLQPEMSAYEVTDALVEDIKNDKHDAIILNFANPDMVGHSGMLEPTIKAIE 418

Qy        422 ATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPFTCSSKTFVFK 481
Db        419 AVDENLGRVVDLILEKGGSAIIFADHGNSETMSTPEGKPHTAHTTVPVPVIVTKK----- 473

Qy        482 STPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMDGVPLLEQ 524
Db        474 -----GVTLREGGR-LADVAPTMLDLLGVKKPAEMTGESLIQK 510
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RESULT 2

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AAW98438
ID   AAW98438 standard; Protein; 491 AA.
XX
AC   AAW98438;
XX
DT   31-MAR-1999  (first entry)
XX
DE   H. pylori GHPO 476 protein.
XX
KW   GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW   peptic ulcer disease.
XX
OS   Helicobacter pylori.
XX
PN   WO9843478-A1.
XX
PD   08-OCT-1998.
XX
PF   01-APR-1998;   98WO-US06371.
XX
PR   29-JUL-1997;   97US-0902615.
PR   01-APR-1997;   97US-0833457.
PR   24-JUN-1997;   97US-0881227.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
XX
PI   Al-Garawi A,  Kleanthous H,  Miller C,  Oomen RP,  Tomb J;
XX
DR   WPI; 1998-542293/46.
DR   N-PSDB; AAX14157.
XX
PT   New isolated Helicobacter polynucleotides - used to develop products
PT   for the diagnosis, prevention and treatment of Helicobacter
PT   infections and gastrointestinal diseases
XX
PS   Claim 8; Page 748-751; 2054pp; English.
XX
CC   This sequence represents a Helicobacter pylori GHPO protein of the
CC   invention. The polypeptides can be used for preventing or treating
CC   Helicobacter infections, and gastroduodenal diseases associated with
CC   these infections, including acute, chronic, and atrophic gastritis, and
CC   peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC   used for the production of antibodies. The products can also be used for
CC   detection and diagnosis.
XX
SQ   Sequence   491 AA;
```

Query Match 35.8%; Score 996; DB 19; Length 491;
Best Local Similarity 42.9%; Pred. No. 1.4e-90;
Matches 219; Conservative 94; Mismatches 170; Indels 28; Gaps 12;

```
Qy          9 QKVCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG-NWQKLEAHGLHVGLPEGLMGNSE 67
Db          3 QKTLLIITDGIGYRKDSDHNAFFHAKKPTYDLMFKTLPYSLIDTHGLSVGLPKGQMGNSE 62

Qy         68 VGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGVH 127
Db         63 VGHMCIGAGRVLYQDLVKISLSLSLQNDELKNNPAFLNTIQK----SPVVHLMGLMSDGGVH 118

Qy        128 SHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKYGELATIT 187
Db        119 SHIEHFIALALECEKSH-KKVCLHLITDGRDVAPKSALTYLKQ-MQNICNESI-QIATIS 175

Qy        188 GRYYAMDRDKRWERIKMAYEAIVGGIGQKATVDKAVDVVRERYAQSETDEFLKPIVFSDD 247
Db        176 GRFYAMDRDKRFERIELAYHSL---MGLNHTPLSPSEYIQSQYDKNITDEFIMPACFKNY 232

Qy        248 GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYNKEFPFPS 307
Db        233 CGMQDDESFIFINFRNDRARE IVSALGQKQFSGFKRQV--FKKLHIATMTPYDNTFPYPV 290

Qy        308 LFPPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQDEERCMVPSPKEV 367
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                ||| : | ||| ::  :|| | |||||| ||||| ||| |  |::| | :: ||| |
Db        291 LFPKESVQNTLAEVVSQHNLTQSHIAETEKYAHVTFFINGGVETPFKNENRVLIQSPK-V 349

Qy        368 ATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQATDEAI 427
              |||||||:|  |   ::||:: |   |:: |||  ||||||| || :||| :| |  :
Db        350 TTYDLKPEMSAKEVTLAVLEQMKLGT-DLIIVNFANGDMVGHTGNFEASVKAVEAVDACL 408

Qy        428 GKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPFTCSSKTFVFKSTPPTG 487
              |:|    :  :| :::|||||| |:|   : :  | ||        |   ||       |
Db        409 GEILSLAKKLDYAMLLTSDHGNCERMKDENQNPLTNHTAG------SVYCFVL------G 456

Qy        488 DDGKE-RARALRDVAPTVLQLMGLPVPPEMD 517
              |  |  :  || ::| :||:|||| |  ||
Db        457 DGVKSIKNGALNNIASSVLKLMGLKAPATMD 487


RESULT 3
AAG82563
ID   AAG82563 standard; Protein; 505 AA.
XX
AC   AAG82563;
XX
DT   03-SEP-2001  (first entry)
XX
DE   S. epidermidis open reading frame protein sequence SEQ ID NO:2220.
XX
KW   Staphylococcus epidermidis SR1 strain; infection; diagnosis;
KW   vaccination; endocarditis.
XX
OS   Staphylococcus epidermidis.
XX
PN   WO200134809-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30782.
XX
PR   09-NOV-1999;   99US-0164258.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Kimmerly WJ;
XX
DR   WPI; 2001-316495/33.
DR   N-PSDB; AAH53413.
XX
PT   Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT   useful for vaccinating against infections, e.g. endocarditis -
XX
PS   Claim 18; Page 595; 2188pp; English.
XX
CC   AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC   (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC   (I) and (II) can have antibacterial activity and therefore can be used
CC   in vaccination. The nucleic acids (I) may be used to produce the
CC   S. epidermidis polypeptides (II) via the production of vectors
CC   containing them which are used to produce hosts cells which express the
CC   polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC   used to vaccinate subjects and to raise antibodies against the bacteria.
CC   The polypeptides may also be used to assay for other inhibitors of their
CC   activity and therefore identify compounds that may be used for the
CC   treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC   AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC   polynucleotide sequences from the present invention. AAH55091 to
CC   AAH55098 represent oligonucleotide sequences and primers which are used
CC   in the exemplification of the present invention.
CC   N.B. The present invention specifically claims all the polynucleotide
CC   sequences given in the sequence listing of the present specification,
CC   however the sequence listing only goes up to SEQ ID NO:4454 so even
CC   though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC   no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ   Sequence   505 AA;

  Query Match             35.6%;  Score 992;  DB 22;  Length 505;
  Best Local Similarity   39.2%;  Pred. No. 3.6e-90;
  Matches  205;  Conservative   94;  Mismatches  196;  Indels   28;  Gaps    8;

Qy          8 QQKVCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSGNWQK-----LEAHGLHVGLPEGL 62
              :|   |:::||: . : .:|||| :|  |  |:     ::|     :|| || ||||||
Db          3 KQPTALIILDGFANRESEHGNAVKQAHKPNFDRY----YEKYPTTQIEASGLDVGLPEGQ 58

Qy         63 MGNSEVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVS 122
              ||||||||:||||||::|| : ||| :::  ||  |  :  : :  |     ||: ||:|
Db         59 MGNSEVGHMNIGAGRIVYQSLTRINKSIEDGEFFDNTVLNNAVKHVKDNGSALHVFGLLS 118

Qy        123 DGGVHSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKYGE 182
              ||||||| ||||::   |:  : ||::| | ||||    |   |:|:          |:
Db        119 DGGVHSHYKHLFAILELAKKQGIDKVYVHAFLDGRDVDQKSALKYIEETEDKFKELGVGQ 178

Qy        183 LATITGRYYAMDRDKRWERIKMAYEAIVGGIGQKATVDKAVDVVRERYAQSETDEFLKPI 242
              |:::|||||||||||||:| : || ||    |   |  ||   |   |    ||||::|
Db        179 FASVSGRYYAMDRDKRWDREERAYNAIRNFEGPTFTSAKA--GVEANYKNDVTDEFVEPF 236

Qy        243 VF--SDDGRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYN 300
              :    :|| | | | :||:|:| ||  |: |    : :      |    |:  :  |:||
Db        237 IVEGQNDG-VNDGDAVIFYNFRPDRAAQLSEIFTNKAFDGF--KVEQVDNLFYATFTKYN 293

Qy        301 KEFPFPSLFPPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQDEERCM 360
                    :|  |   | : |     |: |   ||||||||||:| :|||  :|: | | :
Db        294 DNVDAEIVFEKVDLNNTIGEVAQDNGLKQLRIAETEKYPHVTYFMSGGRNEEFEGERRRL 353

Qy        361 VPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKAC 420
              : ||| ||||||||||:|  | : ::|::: |   |:: ||| |||||:|  || :||
Db        354 IDSPK-VATYDLKPEMSAYEVKDALLEELDKGDLDLILLNFANPDMVGHSGMLEPTIKAI 412

Qy        421 QATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPFTCSSKTFVF 480
              :| || :|:: :          ::|:|||:::::  |    | || | ||    : :
Db        413 EAVDECLGEVVDKIIDMGGHAIITADHGNSDQVLTDDDQPMTTHTTNPVPVIVTKEGVTL 472

Qy        481 KSTPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMDGVPLLE 523
              : |   |           |:|||:| |: :  | || |  |::
Db        473 RETGRLG----------DLAPTLLDLLNVKQPSEMTGESLIK 504


RESULT 4
ABP40599
ID   ABP40599 standard; Protein; 517 AA.
XX
AC   ABP40599;
XX
DT   24-JUL-2002  (first entry)
XX
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5444.
XX
KW   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW   antibacterial; gene therapy.
XX
OS   Staphylococcus epidermidis.
XX
PN   US6380370-B1.
XX
PD   30-APR-2002.
XX
PF   13-AUG-1998;   98US-0134001.
XX
PR   14-AUG-1997;   97US-055779P.
PR   08-NOV-1997;   97US-064964P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2002-381255/41.
DR   N-PSDB; ABN93144.
XX
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```
PT   Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT . polypeptide, useful for diagnosing and treating bacterial infections -
XX
PS   Disclosure; SEQ ID 5444; 267pp; English.
XX
CC   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC   frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC   given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC   antibacterial activity and can be used in gene therapy. The sequences
CC   can also be used in the diagnosis and treatment of bacterial infections,
CC   particularly S. epidermidis infections. The sequences can be used to
CC   screen for compounds able to interfere with the S. epidermidis life
CC   cycle or inhibit S. epidermidis infection.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   USPTO web site.
XX
SQ   Sequence   517 AA;

  Query Match             35.6%;  Score 992;  DB 23;  Length 517;
  Best Local Similarity   39.2%;  Pred. No. 3.7e-90;
  Matches  205;  Conservative   94;  Mismatches  196;  Indels   28;  Gaps    8;

Qy          8 QQKVCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSGNWQK-----LEAHGLHVGLPEGL 62
              :|   |:::||:   : :||||: :|  |  |:     ::|     :|| || ||||||
Db         15 KQPTALIILDGFANRESEHGNAVKQAHKPNFDRY----YEKYPTTQIEASGLDVGLPEGQ 70

Qy         63 MGNSEVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVS 122
              ||||||||:||||||::|| : ||| :::  ||  |  :  : :  |      ||: ||:|
Db         71 MGNSEVGHMNIGAGRIVYQSLTRINKSIEDGEFFDNTVLNNTVKHVKDNGSALHVFGLLS 130

Qy        123 DGGVHSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKYGE 182
              |||||||  ||||::   |:  : ||::| | ||||    |   |:|:          |:
Db        131 DGGVHSHYKHLFAILELAKKQGIDKVYVHAFLDGRDVDQKSALKYIEETEDKFKELGVGQ 190

Qy        183 LATITGRYYAMDRDKRWERIKMAYEAIVGGIGQKATVDKAVDVVRERYAQSETDEFLKPI 242
              |:::||||||||||||:| : || ||    |   |  ||  |   |   ||||::|
Db        191 FASVSGRYYAMDRDKRWDREERAYNAIRNFEGPTFTSAKA--GVEANYKNDVTDEFVEPF 248

Qy        243 VF--SDDGRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYN 300
              :    :|| | | | :||:|:| ||  |: |    : :      |    |:  :  |:||
Db        249 IVEGQNDG-VNDGDAVIFYNFRPDRAAQLSEIFTNKAFDGF--KVEQVDNLFYATFTKYN 305

Qy        301 KEFPFPSLFPPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQDEERCM 360
                    :|  |   | : |     |: |   ||||||||||:| :|||  :|: | | :
Db        306 DNVDAEIVFEKVDLNNTIGEVAQDNGLKQLRIAETEKYPHVTYFMSGGRNEEFEGERRRL 365

Qy        361 VPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKAC 420
              : ||| |||||||||:|  | : ::|::: |   |:: ||| ||||||:|  || :||
Db        366 IDSPK-VATYDLKPEMSAYEVKDALLEELDKGDLDLILLNFANPDMVGHSGMLEPTIKAI 424

Qy        421 QATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPFTCSSKTFVF 480
              :| || :|:: :         ::|:||||:::::  |    | || | ||   : :
Db        425 EAVDECLGEVVDKIIDMGGHAIITADHGNSDQVLTDDDQPMTTHTTNPVPVIVTKEGVTL 484

Qy        481 KSTPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMDGVPLLE 523
              : |   |           |:|||:| |: :  | || |  |::
Db        485 RETGRLG----------DLAPTLLDLLNVKQPSEMTGESLIK 516


RESULT 5
AAW28504
ID   AAW28504 standard; Protein; 557 AA.
XX
AC   AAW28504;
XX
DT   07-JAN-1998  (first entry)
XX
DE   Mugwort grass pollen co-factor-independent phosphoglycerate mutase
DE   isoform Art6.
XX
KW   Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW   Mugwort; pollen; allergy; plant allergen; panallergen; B cell;
KW   T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW   conserved.
XX
OS   Artemisia vulgaris.
XX
PN   WO9705258-A2.
XX
PD   13-FEB-1997.
XX
PF   02-AUG-1996;   96WO-AT00141.
XX
PR   02-AUG-1995;   95AT-0001320.
XX
PA   (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI   Breitenbach M,  Ebner C,  Engel E, Ferreira F,  Jilek A;
PI   Kraft D,  Richter K,  Rheinberger H;
XX
DR   WPI; 1997-145695/13.
DR   N-PSDB; AAT86245.
XX
PT   New recombinant DNA encoding plant phospho:glycerate mutase or its
PT   antigenic epitope(s) - useful for diagnosis or treatment of
PT   allergies to pollen and plant-derived foods
XX
PS   Claim 1; Fig 10a; 160pp; German.
XX
CC   AAW28504 represents mugwort pollen co-factor-independent
CC   phosphoglycerate mutase (PGM-i) isoform Art6. PGM-i is a highly conserved
CC   plant allergen (panallergen) which can cause cross-reactivity in patients
CC   allergic to pollen and plant-derived foods. PGM-i and it's B cell and T
CC   cell epitopes can be used for the in vitro detection of allergy against
CC   PGM-i, by measuring serum IgE or a cellular reaction. They can also be
CC   used in immunotherapy and will not cause an autoimmune response because
CC   PGM-i is significantly different from the human enzyme, which is
CC   co-factor dependent.
XX
SQ   Sequence   557 AA;

  Query Match             26.4%;  Score 736.5;  DB 18;  Length 557;
  Best Local Similarity   35.1%;  Pred. No. 1.8e-64;
  Matches  195;  Conservative   80;  Mismatches  204;  Indels   77;  Gaps   20;

Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNS 66
              | ::|:|||| :     | |  |:|| || | :|   :|: : |||  |||| |  ||||
Db         22 VAMIVLDGWGEASPDKYNCIHVAETPTMDSLKNGAPDHWRLVRAHGTAVGLPTEDDMGNS 81

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQ----------RNEFVTNPQIVASAERAKKGSG 113
              ||||  :||||:  |    :: |:              :  | ||
Db         82 EVGHNALGAGRIFAQGAKLVDQALASGRIYEDEGFNYIKESFATN---------------- 126

Qy        114 RLHLLGLVSDGGVHSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQ 173
              |||:||:|||||| :| |  |:    :   |: :|   ||||    |  |: | |
Db        127 TLHLIGLMSDGGVHSRLDQLQLLLNGASERGAKKIRVHVLTDGRDVLDGSSVGFAETLEA 186

Qy        174 FIASEKY----GELATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQK-ATVDKAVDV 225
              :|| :      ::|:  || |  ||| :  || :|: ::| ::|    |   | :|:
Db        187 ELASLRSKGIDAQVASGGGRMYVTMDRYENDWEVVKLGWDAQVLGEAPHKFKNVVEAIKT 246

Qy        226 VRERYAQSETDEFLKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKD 280
              :|:  |    |::| | |  ||      | | | | ::  |:|||||  : : |  |:: |
Db        247 LRQ--APGANDQYLPPFVIVDDSGTPVGPVVDGDAVVTVNFRADRMTMLAQALEYEKF-D 303

Qy        281 LNSSVPHPKNIQISGMTQYNKEFPFPS--LFPPVTHTNVLAEWLASQGVTQFHCAETEKY 338
                |  || |: :|| ||: |  . |:  |  |         |:|   ||  | |:|| |:
Db        304 KFDRVRFPK-IRYAGMLQYDGELKLPNHYLVSPPLIDRTSGEYLVHNGVRTFACSETVKF 362

Qy        339 PHVTFFFNGGREVQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPL 396
              |||||:|| |   |    ||   :||   : |:::||:| |  : ||  : | ||:
Db        363 GHVTFFWNGNRSGYFNSELEEYVEIPSDSGI-TFNVKPKMKALEIGEKTRDAILSGKFDQ 421

Qy        397 VMCNFAPPDMVGHTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMI-- 454
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Db        422 VRVNIPNGDMVGHTGDVEATVVACKAADEAVKMILDAVEQVGGIYVVTADHGNAEDMVKR 481

Qy        455 -------APDGSEH--TAHTCNLVPFTCS----SKTFVFKSTPPTGDDGKERARALRDVA 501
                  ||     |:||   ||        |    |:   |:|         | :||
Db        482 NKKGEPLLKDGEVQILTSHTLQPVPIAIGGPGLSAGVRFRKDVPSG--------GLANVA 533

Qy        502 PTVLQLMGLPVPPEMD 517
                ||: | |    | : :
Db        534 ATVMNLHGFVAPEDYE 549
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RESULT 6
AAG38644
ID AAG38644 standard; Protein; 560 AA.
XX
AC AAG38644;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47704.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match           26.2%;  Score 729;  DB 21;  Length 560;
  Best Local Similarity  34.9%;  Pred. No. 1e-63;
  Matches  192;  Conservative   89;  Mismatches  201;  Indels   68;  Gaps   21;

Qy         13 LVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNSEV 68
               |:|:|||| ||    | | || || || | |    |: ::|||  |||| |  |||||
Db         25 LIVLDGWGESDPDQYNCIHKAPTPAMDSLKDGKPDTWRLIKAHGTAVGLPSEDDMGNSEV 84

Qy         69 GHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGVHS 128
              ||  :|||:  |    ::||:   :   :      ::  :||:  :||:||:||||||
Db         85 GHNALGAGRIYAQGAKLVDLALASGKIYEDEGFKYISQSFEKGT--VHLIGLLSDGGVHS 142

Qy        129 HIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKY----GELA 184
              :| :  |:: | :    :: :|   ||||    |  |::| |   :|: :      ::|
Db        143 RLDQVQLLLKGFAERGAKRIRVHILTDGRDVLDGSSVGFVETLEADLAALRAKGVDAQVA 202

Qy        185 TITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRERYAQ-SETDEFLK 240
              :  || |  ||| :  |  :|  ::| ::|    |     |:: |:  |:    |::|
Db        203 SGGGRMYVTMDRYENDWSVVKRGWDAQVLGEAPHK--FKSALEAVKTLRAEPGANDQYLP 260

Qy        241 PIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNS----SVPHPKNI 291
               |  ||     | : | | :: ||:|||||    : |    ||| :      ||   :|
Db        261 SFVIVDDNGKAVGPIVDGDAVVTFNFRADRMVMHAKAL---EYKDFDKFDRVRVP---DI 314

Qy        292 QISGMTQYNKEFPFPSLF---PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGG 348
              : :|| ||: |   || :   ||:       |:||  ||  | |:|| |: |||||:||
Db        315 RYAGMLQYDGELKLPSRYLVSPPLI-DRTSGEYLAHNGVRTFACSETVKFGHVTFFWNGN 373

Qy        349 REVQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDM 406
              |   | :  ||   :||   : :::::|:| |  :|||  : | ||:  |  |    ||
Db        374 RSGYFNEKLEEYVEIPSDSGI-SFNVQPKMKALEIAEKARDAILSGKFDQVRVNLPNGDM 432

Qy        407 VGHTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH----- 461
              |||||  |  | ||:| | |:  | :| :    : :||:|||||| |:  | |
Db        433 VGHTGDIEATVVACEAADRAVRTILDAIEQVGGIYVVTADHGNAEDMVKRDKSGKPALDK 492

Qy        462 -------TAHTCNLVPFTCS----SKTFVFK---STPPTGDDGKERARALRDVAPTVLQL 507
                    |:||   ||        |    |:    ||              | :|| ||: |
Db        493 EGNLQILTSHTLKPVPIAIGGPGLSAGVRFRQDIETP----------GLANVAATVMNL 541

Qy        508 MGLPVPPEMD 517
               |   | : :
Db        542 HGFVAPSDYE 551
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RESULT 7
AAG26479
ID   AAG26479 standard; Protein; 557 AA.
XX
AC   AAG26479;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 30950.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
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PR   29-MAR-1999;   99US-0126785.
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PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.

PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 25.3%; Score 706; DB 21; Length 557;
Best Local Similarity 34.4%; Pred. No. 2.1e-61;
Matches 189; Conservative 85; Mismatches 213; Indels 62; Gaps 21;

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Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNS 66
              : ::|:|||| |     | |  | || || |  |     |  ::|||  |||| |  ||||
Db         21 IAVIVLDGWGESAPDQYNCIHNAPTPAMDSLKHGAPDTWTLIKAHGTAVGLPSEDDMGNS 80

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGV 126
              ||||  :||||:  |    : |:    .  .:|  :  :  |||:||:|||||
Db         81 EVGHNALGAGRIFAQGAKLCDQALASGKIFEGEGEFKYVSESFE--TNTLHLVGLLSDGGV 138

Qy        127 HSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQL-LQFIASEKYG---E 182
              || :| |  ||:   :    :: :|   ||||    |  |::| |    :|  : |   :
Db        139 HSRLDQLQLLIKGSAERGAKRIRVHILTDGRDVLDGSSVGFVETLEADLVALRENGVDAQ 198

Qy        183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRE-RYAQSETDEF 238
              :|:  || |  :|| :  || :|  ::| ::|    |     ||: |:  |      |::
Db        199 IASGGGRMYVTLDRYENDWEVVKRGWDAQVLGEAPHK--FKNAVEAVKTLRKEPGANDQY 256

Qy        239 LKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQI 293
              | | |  |:     | : | | :: ||:|||||    : |  | : |    | :|| |:
Db        257 LPPFVIVDESGKAVGPIVDGDAVVTFNFRADRMVMHAKALEYEDF-DKFDRVRYPK-IRY 314

Qy        294 SGMTQYNKEFPFPSLF----PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGR 349
              :|| ||: |   || :    | :  |:   |:|   ||: | |:|| |: |||||:|| |
Db        315 AGMLQYDGELKLPSRYLVSPPEIDRTS--GEYLTHNGVSTFACSETVKFGHVTFFWNGNR 372

Qy        350 EVQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMV 407
                 | :  ||   :||   : :::::|:| |  : ||  :  | ||:   |  |    |||
Db        373 SGYFNEKLEEYVEIPSDSGI-SFNVQPKMKALEIGEKARDAILSGKFDQVRVNIPNGDMV 431

Qy        408 GHTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH------ 461
              ||||  |  | ||:| | |:  ||:| :    : :||:|||||| |:  | |
Db        432 GHTGDIEATVVACEAADLAVKMIFDAIEQVKGIYVVTADHGNAEDMVKRDKSGKPALDKE 491

Qy        462 ------TAHTCNLVPFTCSSKTFV----FK---STPPTGDDGKERARALRDVAPTVLQLM 508
                   |:||   ||           |:   ||           | :|| ||: |
Db        492 GKLQILTSHTLKPVPIAIGGPGLAQGVRFRKDLETP----------GLANVAATVMNLH 540

Qy        509 GLPVPPEMD 517
              |   | : :
Db        541 GFVAPSDYE 549
```

RESULT 8
AAW28505
ID AAW28505 standard; Protein; 560 AA.
XX
AC AAW28505;
XX
DT 07-JAN-1998 (first entry)
XX
DE Mugwort grass pollen co-factor-independent phosphoglycerate mutase
DE isoform Art17.
XX
KW Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Mugwort; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW conserved.
XX
OS Artemisia vulgaris.
XX
PN WO9705258-A2.
XX
PD 13-FEB-1997.
XX
PF 02-AUG-1996; 96WO-AT00141.
XX
PR 02-AUG-1995; 95AT-0001320.
XX
PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
XX
DR WPI; 1997-145695/13.
DR N-PSDB; AAT86246.
XX
PT New recombinant DNA encoding plant phospho:glycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
XX
PS Claim 1; Fig 10b; 160pp; German.
XX
CC AAW28505 represents mugwort pollen co-factor-independent
CC phosphoglycerate mutase (PGM-i) isoform Art17. PGM-i is a highly
CC conserved plant allergen (panallergen) which can cause cross-reactivity
CC in patients allergic to pollen and plant-derived foods. PGM-i and it's B
CC cell and T cell epitopes can be used for the in vitro detection of
CC allergy against PGM-i, by measuring serum IgE or a cellular reaction.
CC They can also be used in immunotherapy and will not cause an autoimmune
CC response because PGM-i is significantly different from the human enzyme,
CC which is co-factor dependent.
XX
SQ Sequence 560 AA;

Query Match 25.2%; Score 703; DB 18; Length 560;
Best Local Similarity 33.4%; Pred. No. 4.2e-61;
Matches 182; Conservative 95; Mismatches 214; Indels 54; Gaps 20;

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Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKL---CSGNWQKLEAHGLHVGLP-EGLMGNS 66
              : :||:|||| :     | |  |:||:|  |     :|: : |||  |||| :  ||||
Db         24 IAVVVLDGWGEASPDKYNCIHVAQTPVMYSLKNSAPDHWRLVRAHGTAVGLPTDDDMGNS 83

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGV 126
              ||||  :||||:  |    ::||:  :  :    :  :    : |||:||:|||||
Db         84 EVGHNALGAGRIYAQGAKLVDLALASGKIYDDEGF--NYIKESFANNTLHLIGLMSDGGV 141

Qy        127 HSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIASEKY----GE 182
              || :| |  |::   :    |: :|   ||||    |  |: | | : :|  :      :
Db        142 HSRLDQLQLLLKGASERGAKKIRVHVLTDGRDVLDGSSVGFAETLEKDLADLRSKGIDAQ 201

Qy        183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRE-RYAQSETDEF 238
              :|:  || |  ||| :  |: :|  ::| ::|    |     ||: ::: | | :  |::
Db        202 VASGGGRMYVTMDRYENDWDVVKRGWDAQVLGEAPHK--FKSAVEAIKKLREAPNANDQY 259

Qy        239 LKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQI 293
              | | |  |:     | : | | :: ||:|||||  : : |  |:: |    |  || |:
Db        260 LPPFVIVDESGKPVGPIMDGDAVVTFNFRADRMTILAQALEYEKF-DKFDRVRFPK-IRY 317

Qy        294 SGMTQYNKEFPFPSLF---PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGRE 350
```

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           :|| ||: |   || :   ||:       |:| : |:  | |:|| |: ||||:|| |
Db        318 AGMLQYDGELKLPSRYLVSPPLIE-RTSGEYLVNNGIRTFACSETVKFGHVTFFWNGNRS 376

Qy        351 VQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVG 408
              |    ||   :||   : :::::|:| |  : ||  : | | :   |  |    ||||
Db        377 GYFNSELEEYVEIPSDNGI-SFNVQPKMKALEIGEKARDAILSRKFDQVRVNIPNGDMVG 435

Qy        409 HTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIA----------PDG 458
              |||  |  | ||:| |:|:  | :| :    : :|||:|||||| |:           ||
Db        436 HTGDIEATVVACKAADDAVKMILDAIKEVGGIYVVTADHGNAEDMVKRNKEGEPLLDKDG 495

Qy        459 SEH--TAHTCNLVPFTCSSKTFV----FKSTPPTGDDGKERARALRDVAPTVLQLMGLPV 512
                 |:||   ||           |:   | |         | :|| ||: | |
Db        496 KVQILTSHTLQPVPVAIGGPGLAAGVKFRKDVPNG--------GLANVAATVMNLHGFVA 547

Qy        513 PPEMD 517
              | : :
Db        548 PDDYE 552


RESULT 9
AAW28502
ID   AAW28502 standard; Protein; 556 AA.
XX
AC   AAW28502;
XX
DT   07-JAN-1998  (first entry)
XX
DE   Timothy grass pollen co-factor-independent phosphoglycerate mutase
DE   isoform Phl1.
XX
KW   Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW   Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
KW   T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW   conserved.
XX
OS   Phleum pratense L.
XX
PN   WO9705258-A2.
XX
PD   13-FEB-1997.
XX
PF   02-AUG-1996;   96WO-AT00141.
XX
PR   02-AUG-1995;   95AT-0001320.
XX
PA   (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI   Breitenbach M,  Ebner C,  Engel E, Ferreira F,  Jilek A;
PI   Kraft D,  Richter K,  Rheinberger H;
XX
DR   WPI; 1997-145695/13.
DR   N-PSDB; AAT86243.
XX
PT   New recombinant DNA encoding plant phospho:glycerate mutase or its
PT   antigenic epitope(s) - useful for diagnosis or treatment of
PT   allergies to pollen and plant-derived foods
XX
PS   Claim 1; Fig 7a; 160pp; German.
XX
CC   AAW28502 shows Timothy grass pollen co-factor-independent
CC   phosphoglycerate mutase (PGM-i) isoform Phl1. PGM-i is a highly conserved
CC   plant allergen (panallergen) which can cause cross-reactivity in patients
CC   allergic to pollen and plant-derived foods. PGM-i and it's B cell and T
CC   cell epitopes can be used for the in vitro detection of allergy against
CC   PGM-i, by measuring serum IgE or a cellular reaction. They can also be
CC   used in immunotherapy and will not cause an autoimmune response because
CC   PGM-i is significantly different from the human enzyme, which is
CC   co-factor dependent.
XX
SQ   Sequence   556 AA;

  Query Match             25.0%;  Score 696;  DB 18;  Length 556;
  Best Local Similarity   33.9%;  Pred. No. 2.1e-60;
  Matches  186;  Conservative   92;  Mismatches  210;  Indels   60;  Gaps   21;

Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNS 66
              | ::|:|||| :     | | :|:||:|| | :|    | .::||| |||| :  ||||
Db         19 VAVIVLDGWGEASADQYNCIHRAETPVMDSLKNGAPEKWTLVKAHGTAVGLPSDDDMGNS 78

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGV 126
              ||||  :|||||:  |     : |:   :   :        |   :|:  |||:||:|||||
Db         79 EVGHNALGAGRIFAQGAKLFDAALASGKIWEDEGFNYIKESFAEGT--LHLIGLLSDGGV 136

Qy        127 HSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIAS--EK--YGE 182
              || :| :  |::   :    :: :|   ||||    |  |::| |   :|   ||    :
Db        137 HSRLDQVQLLVKGASERGAKRIRLHILTDGRDVLDGSSVGFVETLENDLAQLREKGVDAQ 196

Qy        183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRERYAQSE-TDEF 238
              :|:  || |  ||| :  |: :|  ::| ::|    |     |:: |:   |: :  |:: .
Db        197 VASGGGRMYVTMDRYENDWDVVKRGWDAQVLGEAPYK--FKSALEAVKTLRAEPKANDQY 254

Qy        239 LKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQI 293
              |   |  |:     | : | | :: ||:|||||  : : |    : |    |  || |:
Db        255 LPAFVIVDESGKSVGPIVDGDAVVIFNFRADRMVMLAKALEFADF-DKFDRVRVPK-IKY 312

Qy        294 SGMTQYNKEFPFPSLF---PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGRE 350
              :|| ||: |   |: |   ||:       |:|   |-|  | |:|| |: |||||:|| |
Db        313 AGMLQYDGELKLPNKFLVSPPLIE-RTSGEYLVKNGVRTFACSETVKFGHVTFFWNGNRS 371

Qy        351 VQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVG 408
                 | :  ||   :||   : |:: :|:| |  :|||  : | ||:   |  |    ||||
Db        372 GYFDETKEEYIEIPSDSGI-TFNEQPKMKALEIAEKTRDAILSGKFDQVRINLPNGDMVG 430

Qy        409 HTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH------- 461
              |||  |  | ||:| |||:  : :| :    : :||:|||||| |:  : |
Db        431 HTGDIEATVVACKAADEAVKIVLDAVEQVGGIYLVTADHGNAEDMVKRNKSGQPALDKSG 490

Qy        462 -----TAHTCNLVPFTCSSKTF----VFKS---TPPTGDDGKERARALRDVAPTVLQLMG 509
                    |:||   ||           |:|   ||          | :|| ||: | |
Db        491 SIQILTSHTLQPVPVAIGGPGLHPGVKFRSDINTP----------GLANVAATVMNLHG 539

Qy        510 LPVPPEMD 517
                 | : :
Db        540 FQAPDDYE 547


RESULT 10
AAW28503
ID   AAW28503 standard; Protein; 555 AA.
XX
AC   AAW28503;
XX
DT   07-JAN-1998  (first entry)
XX
DE   Timothy grass pollen co-factor-independent phosphoglycerate mutase
DE   isoform Phl5.
XX
KW   Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW   Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
KW   T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW   conserved.
XX
OS   Phleum pratense L.
XX
PN   WO9705258-A2.
XX
PD   13-FEB-1997.
XX
PF   02-AUG-1996;   96WO-AT00141.
XX
PR   02-AUG-1995;   95AT-0001320.
XX
PA   (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI   Breitenbach M,  Ebner C,  Engel E, Ferreira F,  Jilek A;
```

```
PI   Kraft D,  Richter K,  Rheinberger H;
XX
DR   WPI; 1997-145695/13.
DR   N-PSDB; AAT86244.
XX
PT   New recombinant DNA encoding plant phospho:glycerate mutase or its
PT   antigenic epitope(s) - useful for diagnosis or treatment of
PT   allergies to pollen and plant-derived foods
XX
PS   Claim 1; Fig 7b; 160pp; German.
XX
CC   AAW28503 shows Timothy grass pollen co-factor-independent
CC   phosphoglycerate mutase (PGM-i) isoform Phl5. PGM-i is a highly conserved
CC   plant allergen (panallergen) which can cause cross-reactivity in patients
CC   allergic to pollen and plant-derived foods. PGM-i and it's B cell and T
CC   cell epitopes can be used for the in vitro detection of allergy against
CC   PGM-i, by measuring serum IgE or a cellular reaction. They can also be
CC   used in immunotherapy and will not cause an autoimmune response because
CC   PGM-i is significantly different from the human enzyme, which is
CC   co-factor dependent.
XX
SQ   Sequence   555 AA;

  Query Match             24.9%;  Score 694;  DB 18;  Length 555;
  Best Local Similarity   33.9%;  Pred. No. 3.3e-60;
  Matches  186;  Conservative   92;  Mismatches  210;  Indels   60;  Gaps   21;

Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNS 66
              | ::|:|||| :     | | :|:||:|| | :|    |  ::|||  |||| :  ||||
Db         18 VAVIVLDGWGEASADQYNCIHRAETPVMDSLKNGAPEKWTLVKAHGTAVGLPSDDDMGNS 77

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGV 126
              ||||  :||||:  |     : |:   :   :       |   :|:  |||:||:|||||
Db         78 EVGHNALGAGRIFAQGAKLFDAALASGKIWEDEGFNYIKESFAEGT--LHLIGLLSDGGV 135

Qy        127 HSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIAS--EK--YGE 182
              || :| :  |::   :    :: :|   ||||    |  |::| |   :|  ||    :
Db        136 HSRLDQVQLLVKGASERGAKRIRLHILTDGRDVLDGSSVGFVETLENDLAQLREKGVDAQ 195

Qy        183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRERYAQSE-TDEF 238
              :|:  || |  ||| :  |: :|  ::| ::|    |     |:: |:   |: :  |::
Db        196 VASGGGRMYVTMDRYENDWDVVKRGWDAQVLGEAPYK--FKSALEAVKTLRAEPKANDQY 253

Qy        239 LKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQI 293
              |   |  |:     | : | | :: ||:|||||  : : |    : |    |  || |:
Db        254 LPAFVIVDESGKSVGPIVDGDAVVTFNFRADRMVMLAKALEFADF-DKFDRVRVPK-IKY 311

Qy        294 SGMTQYNKEFPFPSLF---PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGRE 350
              :|| ||: |   |: |   ||:       |:|   ||  | |:|| |: ||||:|| |
Db        312 AGMLQYDGELKLPNKFLVSPPLIE-RTSGEYLVKNGVRTFACSETVKFGHVTFFWNGNRS 370

Qy        351 VQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVG 408
              | :  ||   :||   : |:: :|:| |  :|||  : | ||:   |  |    ||||
Db        371 GYFDETKEEYIEIPSDSGI-TFNEQPKMKALEIAEKTRDAILSGKFDQVRINLPNGDMVG 429

Qy        409 HTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH------- 461
              |||  |  | ||:| |||:  : :| :    : :||:|||||| |:  : |
Db        430 HTGDIEATVVACKAADEAVKIVLDAVEQVGGIYLVTADHGNAEDMVKRNKSGQPALDKSG 489

Qy        462 -----TAHTCNLVPFTCSSKTF----VFKS---TPPTGDDGKERARALRDVAPTVLQLMG 509
                  |:||   ||             |:|   |'|             | :|| ||: | |
Db        490 SIQILTSHTLQPVPVAIGGPGLHPGVKFRSDINTP-----------GLANVAATVMNLHG 538

Qy        510 LPVPPEMD 517
                | : :
Db        539 FQAPDDYE 546


RESULT 11
AAG30862
ID   AAG30862 standard; Protein; 575 AA.
XX
AC   AAG30862;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36971.
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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PN   EP1033405-A2.
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Best Local Similarity 33.3%; Pred. No. 1.8e-59;
Matches 189; Conservative 85; Mismatches 213; Indels 80; Gaps 22;

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Qy         11 VCLVVIDGWGLSDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHVGLP-EGLMGNS 66
              : ::|:|||| |     | |  | || || |  |    |  ::|||  |||| |  ||||
Db         21 IAVIVLDGWGESAPDQYNCIHNAPTPAMDSLKHGAPDTWTLIKAHGTAVGLPSEDDMGNS 80

Qy         67 EVGHLNIGAGRVIYQDIVRINLAVQRNEFVTNPQIVASAERAKKGSGRLHLLGLVSDGGV 126
              ||||  :||||:  |     : |:  :          :|  :  :  |||:||:|||||
Db         81 EVGHNALGAGRIFAQGAKLCDQALASGKIFEGEGFKYVSESFE--TNTLHLVGLLSDGGV 138

Qy        127 HSHIDHLFALIRAFKQLQVPKVFIHFFADGRDTSPTSGAGYLEQL-LQFIASEKYG---E 182
              || :| |  ||:   :    :: :|   ||||    |  |::| |    :|  : |   :
Db        139 HSRLDQLQLLIKGSAERGAKRIRVHILTDGRDVLDGSSVGFVETLEADLVALRENGVDAQ 198

Qy        183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRE-RYAQSETDEF 238
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Db        199 IASGGGRMYVTLDRYENDWEVVKRGWDAQVLGEAPHK--FKNAVEAVKTLRKEPGANDQY 256

Qy        239 LKPIVFSDD-----GRVKDDDTLIFFNYRADRMRQICECLGLERYKDLNSSVPHPKNIQI 293
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Db        257 LPPFVIVDESGKAVGPIVDGDAVVTFNFRADRMVMHAKALEYEDF-DKFDRVRYPK-IRY 314

Qy        294 SGMTQYNKEFPFPSLF----PPVTHTNVLAEWLASQGVTQFHCA---------------- 333

Db        315 AGMLQYDGELKLPSRYLVSPPEIDRTS--GEYLTHNGVSTFACSSSCLLIIGLYYALHFC 372

Qy        334 --ETEKYPHVTFFFNGGREVQFQD--EERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQI 389

Db        373 QYETVKFGHVTFFWNGNRSGYFNEKLEEYVEIPSDSGI-SFNVQPKMKALEIGEKARDAI 431

Qy        390 ESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQATDEAIGKIFEACQTYNYVLMVTSDHGN 449

Db        432 LSGKFDQVRVNIPNGDMVGHTGDIEATVVACEAADLAVKMIFDAIEQVKGIYVVTADHGN 491

Qy        450 AEKMIAPDGSEH------------TAHTCNLVPFTCSSKTFV----FK---STPPTGDDG 490

Db        492 AEDMVKRDKSGKPALDKEGKLQILTSHTLKPVPIAIGGPGLAQGVRFRKDLETP------ 545

Qy        491 KERARALRDVAPTVLQLMGLPVPPEMD 517

Db        546 -----GLANVAATVMNLHGFVAPSDYE 567
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RESULT 12
AAW28501
ID AAW28501 standard; Protein; 530 AA.
XX
AC AAW28501;
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DT 07-JAN-1998 (first entry)
XX
DE Birch pollen co-factor-independent phosphoglycerate mutase.
XX
KW Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW birch; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW conserved.
XX
OS Betula verrucosa.
XX
PN WO9705258-A2.
XX
PD 13-FEB-1997.
XX
PF 02-AUG-1996; 96WO-AT00141.
XX
PR 02-AUG-1995; 95AT-0001320.
XX
PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
XX
DR WPI; 1997-145695/13.
DR N-PSDB; AAT86242.
XX
PT New recombinant DNA encoding plant phospho:glycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
XX
PS Claim 1; Fig 1; 160pp; German.
XX
CC AAW28501 is a birch pollen co-factor-independent phosphoglycerate
CC mutase (PGM-i). PGM-i is a highly conserved plant allergen (panallergen)
CC which can cause cross-reactivity in patients allergic to pollen and
CC plant-derived foods. PGM-i and it's B cell and T cell epitopes can be
CC used for the in vitro detection of allergy against PGM-i, by measuring
CC serum IgE or a cellular reaction. They can also be used in immunotherapy
CC and will not cause an autoimmune response because PGM-i is significantly
CC different from the human enzyme, which is co-factor dependent.
XX
SQ Sequence 530 AA;

Query Match 24.6%; Score 686; DB 18; Length 530;
Best Local Similarity 36.0%; Pred. No. 1.9e-59;
Matches 191; Conservative 73; Mismatches 208; Indels 58; Gaps 20;

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Qy        144 QVPKVFIHFFADGRDTSPTSGAGYLEQLLQFIAS--EK--YGELATITGR-YYAMDR-DK 197

Db        128 GAKRIRVHILTDGRDVLDGSSVGFVETLENDLAKLREKGVDAQIASGGGRMYVTMDRYEN 187

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Qy        310 ----PPVTHTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQD--EERCMVPS 363

Db        303 LVEPPEIERTS--GEYLVHNGVRTFACSETVKFGHVTFFWNGNRSGYFNSELEEYVEIPS 360

Qy        364 PKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQAT 423

Db        361 DSGI-TFNVQPKMKALEIAEKTRDAILSGKFDQVRVNLPNGDMVGHTGDIEDTVVACKAA 419

Qy        424 DEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH----------TAHTCNLVPF 471

Db        420 DEADKMILDAIEQVGGIYVVTADHGNAEDMVKRNKSVQPLLDKNGNLQVLTSHTLQPVPI 479

Qy        472 TCSSKTFV----FKSTPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMD 517

Db        480 AIGGPALASGVRFCKDLPDG--------GLANVAATVINLHGFEAPSDYE 521
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AC AAG38645;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 47705.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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Db          1 MDSLKDGKPDTWRLIKAHGTAVGLPSEDDMGNSEVGHNALGAGRIYAQGAKLVDLALASG 60

Qy         94 EFVTNPQIVASAERAKKGSGRLHLLGLVSDGGVHSHIDHLFALIRAFKQLQVPKVFIHFF 153
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Db         61 KIYEDEGFKYISQSFEKGT--VHLIGLLSDGGVHSRLDQVQLLLKGFAERGAKRIRVHIL 118

Qy        154 ADGRDTSPTSGAGYLEQLLQFIASEKY----GELATITGR-YYAMDR-DKRWERIKMAYE 207
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Db        119 TDGRDVLDGSSVGFVETLEADLAALRAKGVDAQVASGGGRMYVTMDRYENDWSVVKRGWD 178

Qy        208 A-IVGGIGQKATVDKAVDVVRERYAQ-SETDEFLKPIVFSDD-----GRVKDDDTLIFFN 260
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Db        179 AQVLGEAPHK--FKSALEAVKTLRAEPGANDQYLPSFVIVDDNGKAVGPIVDGDAVVTFN 236

Qy        261 YRADRMRQICECLGLERYKDLNS----SVPHPKNIQISGMTQYNKEFPFPSLF---PPVT 313
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Db        237 FRADRMVMHAKAL---EYKDFDKFDRVRVP---DIRYAGMLQYDGELKLPSRYLVSPPLI 290

Qy        314 HTNVLAEWLASQGVTQFHCAETEKYPHVTFFFNGGREVQFQD--EERCMVPSPKEVATYD 371
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Db        291 -DRTSGEYLAHNGVRTFACSETVKFGHVTFFWNGNRSGYFNEKLEEYVEIPSDSGI-SFN 348

Qy        372 LKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQATDEAIGKIF 431
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Db        349 VQPKMKALEIAEKARDAILSGKFDQVRVNLPNGDMVGHTGDIEATVVACEAADRAVRTIL 408

Qy        432 EACQTYNYVLMVTSDHGNAEKMIAPDGSEH-----------TAHTCNLVPFTCS----S 475
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Db        409 DAIEQVGGIYVVTADHGNAEDMVKRDKSGKPALDKEGNLQILTSHTLKPVPIAIGGPGLS 468

Qy        476 KTFVFK---STPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMD 517
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Db        469 AGVRFRQDIETP----------GLANVAATVMNLHGFVAPSDYE 502


RESULT 14
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DT   17-OCT-2000  (first entry)
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DE   Arabidopsis thaliana protein fragment SEQ ID NO: 30951.
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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OS   Arabidopsis thaliana.
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Best Local Similarity 34.1%; Pred. No. 1.5e-55;
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Qy        154 ADGRDTSPTSGAGYLEQL-LQFIASEKYG---ELATITGR-YYAMDR-DKRWERIKMAYE 207
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Qy        208 A-IVGGIGQKATVDKAVDVVRE-RYAQSETDEFLKPIVFSDD-----GRVKDDDTLIFFN 260
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Db        179 AQVLGEAPHK--FKNAVEAVKTLRKEPGANDQYLPPFVIVDESGKAVGPIVDGDAVVTFN 236

Qy        261 YRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYNKEFPFPSLF----PPVTHTN 316
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Qy        375 EMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAVKACQATDEAIGKIFEAC 434
             :| |  : ||  : | ||:.+|  |    |||||||  |  | ||:| | |:  ||:|
Db        352 KMKALEIGEKARDAILSGKFDQVRVNIPNGDMVGHTGDIEATVVACEAADLAVKMIFDAI 411

Qy        435 QTYNYVLMVTSDHGNAEKMIAPDGSEH-----------TAHTCNLVPFTCSSKTFV--- 479
             :   : :||:|||||| |:  | |              |:||   ||
Db        412 EQVKGIYVVTADHGNAEDMVKRDKSGKPALDKEGKLQILTSHTLKPVPIAIGGPGLAQGV 471

Qy        480 -FK---STPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMD 517
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Db        472 RFRKDLETP----------GLANVAATVMNLHGFVAPSDYE 502
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RESULT 15
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AC AAG30863;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 36972.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 10-SEP-1999; 99US-0153070.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 22.5%; Score 628; DB 21; Length 528;
Best Local Similarity 33.0%; Pred. No. 1.3e-53;
Matches 178; Conservative 81; Mismatches 201; Indels 80; Gaps 22;

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Qy         94 EFVTNPQIVASAERAKKGSGRLHLLGLVSDGGVHSHIDHLFALIRAFKQLQVPKVFIHFF 153
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Db         61 KIFEGEGFKYVSESFE--TNTLHLVGLLSDGGVHSRLDQLQLLIKGSAERGAKRIRVHIL 118

Qy        154 ADGRDTSPTSGAGYLEQL-LQFIASEKYG---ELATITGR-YYAMDR-DKRWERIKMAYE 207
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Db        119 TDGRDVLDGSSVGFVETLEADLVALRENGVDAQIASGGGRMYVTLDRYENDWEVVKRGWD 178

Qy        208 A-IVGGIGQKATVDKAVDVVRE-RYAQSETDEFLKPIVFSDD-----GRVKDDDTLIFFN 260
              | ::|    |     ||: |:  |      |::| | |  |:     | : | | :: ||
Db        179 AQVLGEAPHK--FKNAVEAVKTLRKEPGANDQYLPPFVIVDESGKAVGPIVDGDAVVTFN 236

Qy        261 YRADRMRQICECLGLERYKDLNSSVPHPKNIQISGMTQYNKEFPFPSLF----PPVTHTN 316
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Db        237 FRADRMVMHAKALEYEDF-DKFDRVRYPK-IRYAGMLQYDGELKLPSRYLVSPPEIDRTS 294

Qy        317 VLAEWLASQGVTQFHCA----------------ETEKYPHVTFFFNGGREVQFQD--E 356
                 |:|   ||: | |:                || |: |||||:|| |   | :  |
Db        295 --GEYLTHNGVSTFACSSSCLLIIGLYYALHFCQYETVKFGHVTFFWNGNRSGYFNEKLE 352

Qy        357 ERCMVPSPKEVATYDLKPEMNAAGVAEKMVEQIESGRHPLVMCNFAPPDMVGHTGKFEPA 416
              |   :||   : :::::|:| |  : ||  : | ||:   |  |    |||||||  |
Db        353 EYVEIPSDSGI-SFNVQPKMKALEIGEKARDAILSGKFDQVRVNIPNGDMVGHTGDIEAT 411

Qy        417 VKACQATDEAIGKIFEACQTYNYVLMVTSDHGNAEKMIAPDGSEH-----------TAH 464
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Db        412 VVACEAADLAVKMIFDAIEQVKGIYVVTADHGNAEDMVKRDKSGKPALDKEGKLQILTSH 471

Qy        465 TCNLVPFTCSSKTFV----FK---STPPTGDDGKERARALRDVAPTVLQLMGLPVPPEMD 517
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Search completed: July 31, 2003, 13:32:23
Job time : 86 secs